

Figure 1

Stability Study of SAHH

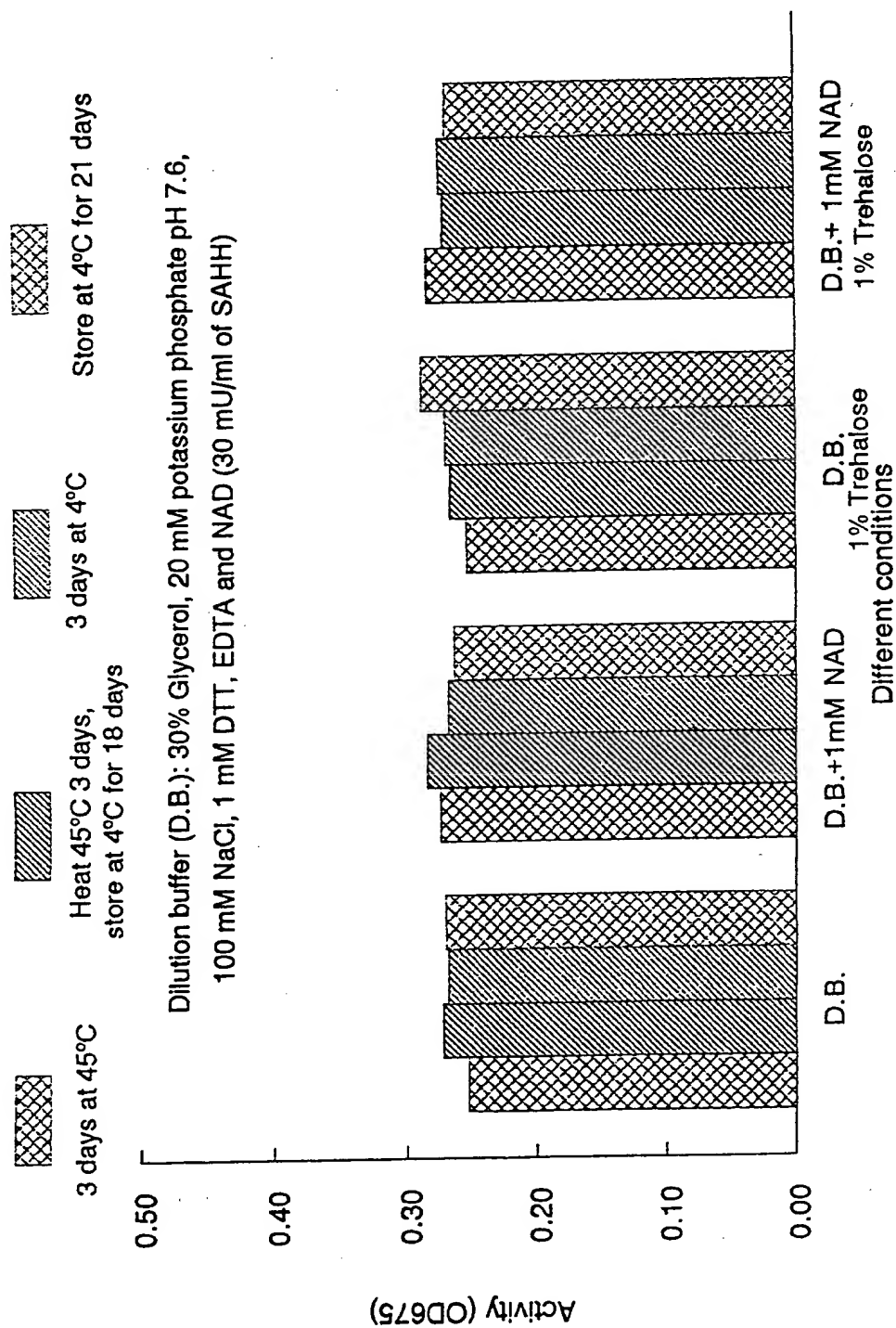


Figure 2

Screening of SAHH

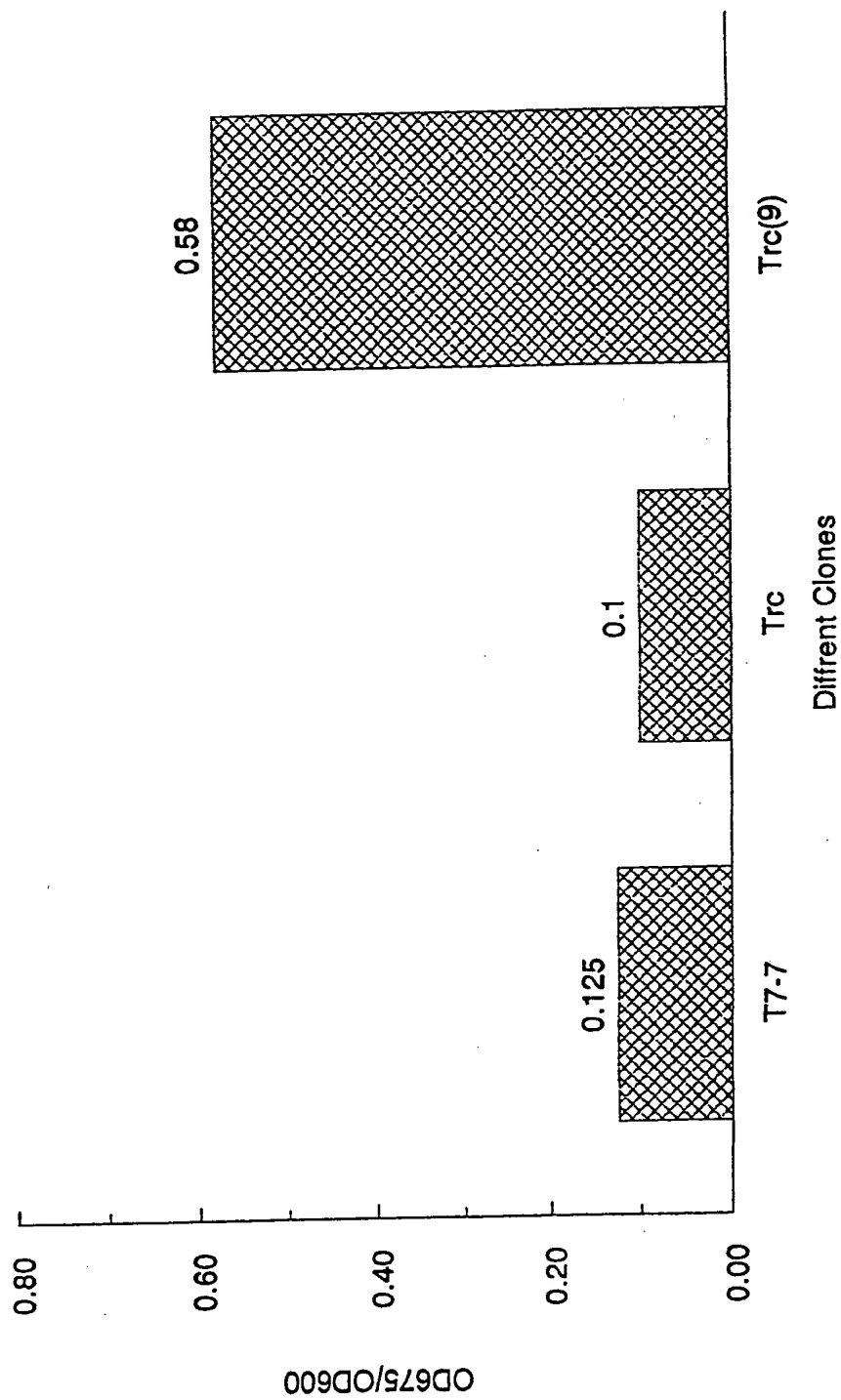


Figure 3

103110-0005/00

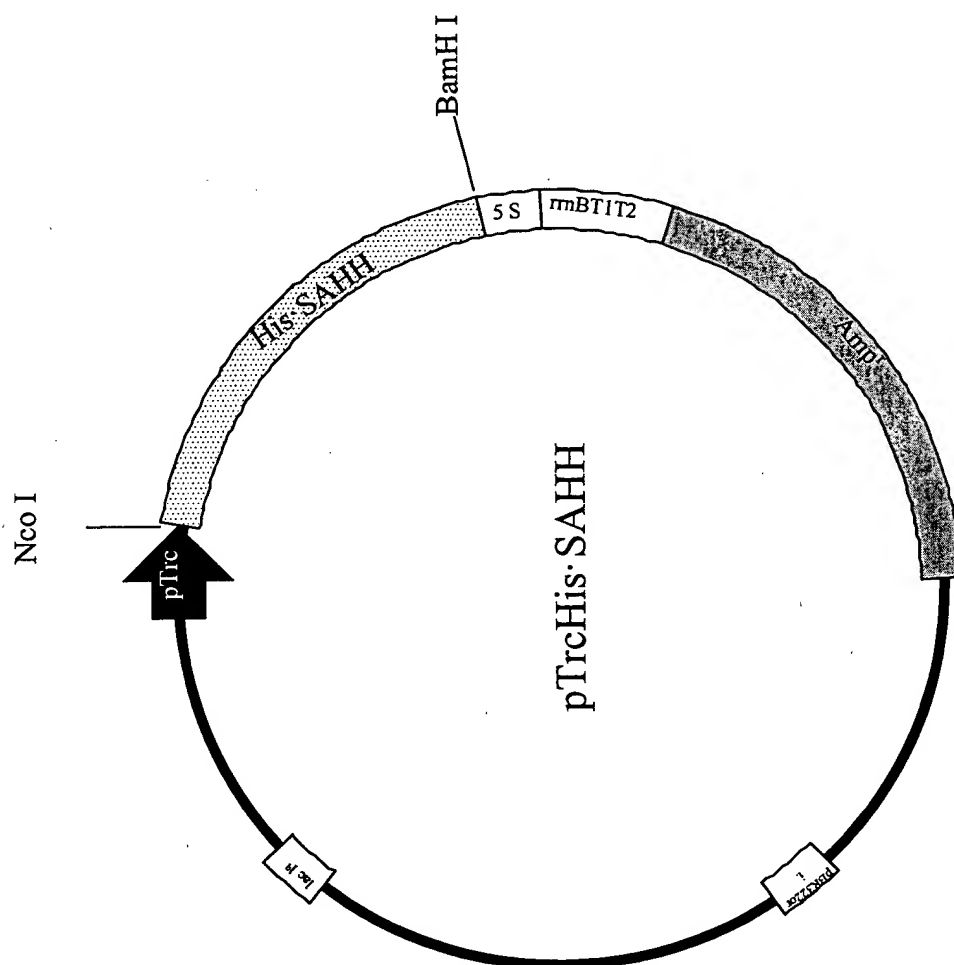


Figure 4

102110-0665/00

Stability of SAHH.His

3 days incubation in different temperature

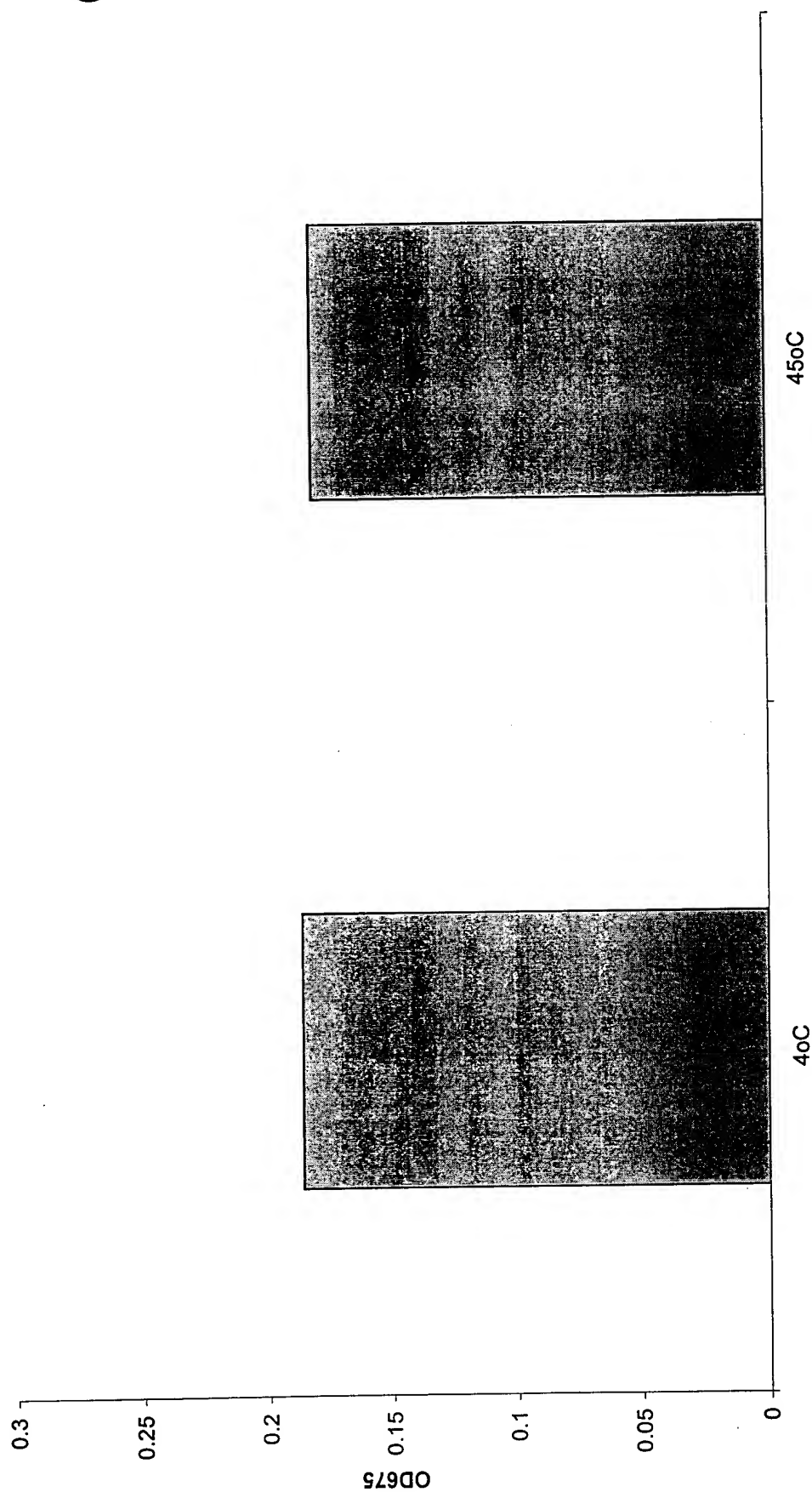


Figure 5

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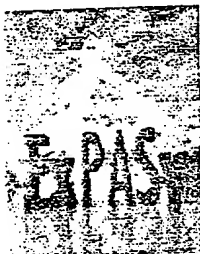
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SIM - Results of the Alignment

Click [here](#) to view these alignments graphically with the [LALNVIEW](#) program (mime-type [chemical/x-aln2](#)).

Click [here](#) to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a [sample screen](#) of LALNVIEW and access its [documentation](#).

Results of SIM with:

Sequence 1: Wild (1882 residues)
Sequence 2: A/C, (1594 residues)

using the parameters:

Number of alignments computed: 20
Cost of a matching aligned pair: 1
Cost of a transition: -1
Cost of a transversion: -1
Gap open penalty: 6.0
Gap extension penalty: 0.2

Accession
GenBank U 408 72
TVU- 40872
Tragalis
deposited
10/31/96

Bagnara, A.S.F.C.
Mil. B. adri. P. adri.
(1996) 81 1-11



Evaluate the significance of this protein sequence similarity score using [PRSS](#) at EMBnet-CH.
new

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

Wild	291	ATGGCTTGCAAATCACCTGCTGGTGCTCCATTGAGTACAGAATTGCCGACATCAACCTC	SEQ ID NO.1
A/C,	71	ATGGCTTGCAAATCACCTACTGGTGCTCCATTGAGTACAGAATTGCCGACATCAACCTC	

Wild	351	CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT	
A/C,	131	CATGTTCTCGGCCGTAAGGAACTTACCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT	

Wild	411	CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTGAGAATCTCTGGTTCCTC	

Figure 6a

```

A/C,      191  CTTCTGTTATTCCGCTTCTAAGCCATTGAAGGGTGTCTATCTCTGGTTCCCTC
*****

Wild
A/C,      471  CACATGACAGTCCAGACAGCGGTCTTATTGAGACACTCACAGCTCTTGGTGCTGATGTC
251  CACATGACAGTCCAGACAGCCGTCTTCATCGAGACACTCACAGCTCTTGGTGCTGATGTC
*****

Wild
A/C,      531  AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
311  AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
*****

Wild
A/C,      591  GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
371  GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCCAGTCTTCGCCTGGAAGGGCGAA
*****

Wild
A/C,      651  ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
431  ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
*****

Wild
A/C,      711  CCACAGCAGGTTGTCGATGATGGTGGTGTGCTACACTCCTCATCTCCAAGGGCTTCGAA
491  CCACAGCAGGTTGTCGATGATGGTGGTGTGCTACACTCCTCATCTCCAAGGGCTTCGAA
*****

Wild
A/C,      771  TTCGAAACAGCCGGTGCTGTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
551  TTCGAAACAGCCGGTGCTGTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
*****

Wild
A/C,      831  GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCCTGGCACACAGTTGCT
611  GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCCTGGCACACAGTTGCT
*****

Wild
A/C,      891  GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCTCTACCAGCTC
671  GCCGGCATGAACGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCTCTACCAGCTC
*****

Wild
A/C,      951  GAGAAGGAGGGCAAACCTCCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
731  GAGAAGGAGGGCAAACCTCCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
*****

Wild
A/C,      1011 AAGTTCGATAACATCTACGGCTGTGCGCACTCCCTTATCGATGGTATCAACCGTGCTTCC
791  AAGTTCGATAACATCTACGGCTGCGCCACTCCCTTATCGATGGTATCAACCGTGCTTCC
*****

Wild
A/C,      1071 GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTACGGCGATGTCGGGAAGGGC
851  GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTACGGCGATGTCGGGAAGGGC
*****

Wild
A/C,      1131 TGCCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCTATC
911  TGCCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCTATC
*****

Wild
A/C,      1191 TGCCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGATCGAGGAAGTCGTCAAG
971  TGCCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGATCGAGGAAGTCGTCAAG
*****

Wild
A/C,      1251 GATGTCGATATCTTCGTTACATGCACAGGAACTGCGATATCATCTCTGTTGACATGATG
1031 GATGTCGATATCTTCGTTACATGCACAGGAACTGCGATATCATCTCTGTTGACATGATG
*****

Wild
A/C,      1311 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
1091 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
*****

Wild
1371 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC

```

Figure 6b

```

A/C,      1151 ACAGATC...CATGAAATACCCAGGCATCAAGCACATCCCA...AGCCAGAATACGAC
          -----
Wild      1431 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
A/C,      1211 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAAC
          *****

Wild      1491 CTTGGTTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTACAAACCAGACA
A/C,      1271 CTTGGCTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTACAAACCAGACA
          *****

Wild      1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTTACACACTT
A/C,      1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTTACACACTT
          *****

Wild      1611 CCGAAGCATCTCGATGAAGAAGTCGTTTCGCTCCACCTCGGATCTCTCGATGTCCACCTT
A/C,      1391 CCGAAGCATCTCGATGAAGAAGTCGTTTCGCTCCACCTCGGATCTCTCGATGTCCACCTT
          *****

Wild      1671 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
A/C,      1451 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
          *****

Wild      1731 TCTGATGCTTACCGTTATTAA
A/C,      1511 TCTGATGCTTACCGTTATTAA
          *****
    
```

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

```

Wild      782 CGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACC
A/C,      682 CGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACC
          *****
    
```

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

```

Wild      1053 GGTATCAACCGTGCTTCCGA
A/C,      674 GGCATGAACGGTGTTCCTGA
          ** ** ** **
    
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```

Wild      564 GATACAGCCGCTGCTG
A/C,      554 GAAACAGCCGGTGCTG
          ** *****
    
```

64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

```

Wild      1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC
A/C,      710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACCTCCTC
          *****
    
```

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

```

Wild      774 GAAACAGCCGGTGCTG
A/C,      344 GATACAGCCGCTGCTG
          ** *****
    
```